



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: WILLIAMS, Lewis T.
ESCOBEDO, Jaime A.
- (ii) TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR RECEPTORS
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Townsend and Townsend and Crew
 - (B) STREET: One Market, Steuart Street Tower, 20th Floor
 - (C) CITY: San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94105
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/461,917
 - (B) FILING DATE: 05-JUN-1995
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/309,322
 - (B) FILING DATE: 10-FEB-1989
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/151,414
 - (B) FILING DATE: 02-FEB-1988
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Dow, Karen B.
 - (B) REGISTRATION NUMBER: 29,684
 - (C) REFERENCE/DOCKET NUMBER: 2307K-267-2-4
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415/326-2400
 - (B) TELEFAX: 415/326-2422

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6373 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 129..3398
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGGAGCTAC AGGGAGAGAA ACAGAGGAGG AGACTGCAAG AGATCATTGG AGGCCGTGGG	60
CACGCTCTTT ACTCCATGTG TGGGACATTC ATTGCGGAAT AACATCGGAG GAGAAGTTTC	120
CCAGAGCT ATG GGG ACT TCC CAT CCG GCG TTC CTG GTC TTA GGC TGT CTT Met Gly Thr Ser His Pro Ala Phe Leu Val Leu Gly Cys Leu 1 5 10	170
CTC ACA GGG CTG AGC CTA ATC CTC TGC CAG CTT TCA TTA CCC TCT ATC Leu Thr Gly Leu Ser Leu Ile Leu Cys Gln Leu Ser Leu Pro Ser Ile 15 20 25 30	218
CTT CCA AAT GAA AAT GAA AAG GTT GTG CAG CTG AAT TCA TCC TTT TCT Leu Pro Asn Glu Asn Glu Lys Val Val Gln Leu Asn Ser Ser Phe Ser 35 40 45	266
CTG AGA TGC TTT GGG GAG AGT GAA GTG AGC TGG CAG TAC CCC ATG TCT Leu Arg Cys Phe Gly Glu Ser Glu Val Ser Trp Gln Tyr Pro Met Ser 50 55 60	314
GAA GAA GAG AGC TCC GAT GTG GAA ATC AGA AAT GAA GAA AAC AAC AGC Glu Glu Glu Ser Ser Asp Val Glu Ile Arg Asn Glu Glu Asn Asn Ser 65 70 75	362
GGC CTT TTT GTG ACG GTC TTG GAA GTG AGC AGT GCC TCG GCG GCC CAC Gly Leu Phe Val Thr Val Leu Glu Val Ser Ser Ala Ser Ala Ala His 80 85 90	410
ACA GGG TTG TAC ACT TGC TAT TAC AAC CAC ACT CAG ACA GAA GAG AAT Thr Gly Leu Tyr Thr Cys Tyr Tyr Asn His Thr Gln Thr Glu Glu Asn 95 100 105 110	458
GAG CTT GAA GGC AGG CAC ATT TAC ATC TAT GTG CCA GAC CCA GAT GTA Glu Leu Glu Gly Arg His Ile Tyr Ile Tyr Val Pro Asp Pro Asp Val 115 120 125	506
GCC TTT GTA CCT CTA GGA ATG ACG GAT TAT TTA GTC ATC GTG GAG GAT Ala Phe Val Pro Leu Gly Met Thr Asp Tyr Leu Val Ile Val Glu Asp 130 135 140	554
GAT GAT TCT GCC ATT ATA CCT TGT CGC ACA ACT GAT CCC GAG ACT CCT Asp Asp Ser Ala Ile Ile Pro Cys Arg Thr Thr Asp Pro Glu Thr Pro 145 150 155	602
GTA ACC TTA CAC AAC AGT GAG GGG GTG GTA CCT GCC TCC TAC GAC AGC Val Thr Leu His Asn Ser Glu Gly Val Val Pro Ala Ser Tyr Asp Ser 160 165 170	650
AGA CAG GGC TTT AAT GGG ACC TTC ACT GTA GGG CCC TAT ATC TGT GAG Arg Gln Gly Phe Asn Gly Thr Phe Thr Val Gly Pro Tyr Ile Cys Glu 175 180 185 190	698
GCC ACC GTC AAA GGA AAG AAG TTC CAG ACC ATC CCA TTT AAT GTT TAT Ala Thr Val Lys Gly Lys Lys Phe Gln Thr Ile Pro Phe Asn Val Tyr 195 200 205	746
GCT TTA AAA GCA ACA TCA GAG CTG GAT CTA GAA ATG GAA GCT CTT AAA Ala Leu Lys Ala Thr Ser Glu Leu Asp Leu Glu Met Glu Ala Leu Lys 210 215 220	794 -
ACC GTG TAT AAG TCA GGG GAA ACG ATT GTG GTC ACC TGT GCT GTT TTT Thr Val Tyr Lys Ser Gly Glu Thr Ile Val Val Thr Cys Ala Val Phe 225 230 235	842
AAC AAT GAG GTG GTT GAC CTT CAA TGG ACT TAC CCT GGA GAA GTG AAA Asn Asn Glu Val Val Asp Leu Gln Trp Thr Tyr Pro Gly Glu Val Lys 240 245 250	890

GGC Gly 255	AAA Lys	GGC Gly	ATC Ile	ACA Thr	ATG Met	CTG Leu	GAA Glu	GAA Glu	ATC Ile	AAA Lys	GTC Val	CCA Pro	TCC Ser	ATC Ile	AAA Lys	938
TTG Leu	GTG Val	TAC Tyr	ACT Thr	TTG Leu	ACG Thr	GTC Val	CCC Pro	GAG Glu	GCC Ala	ACG Thr	GTG Val	AAA Lys	GAC Asp	AGT Ser	GGA Gly	986
GAT Asp	TAC Tyr	GAA Glu	TGT Cys	GCT Ala	GCC Ala	CGC Arg	CAG Gln	GCT Ala	ACC Thr	AGG Arg	GAG Glu	GTC Val	AAA Lys	GAA Glu	ATG Met	1034
AAG Lys	AAA Lys	GTC Val	ACT Thr	ATT Ile	TCT Ser	GTC Val	CAT His	GAG Glu	AAA Lys	GGT Gly	TTC Phe	ATT Ile	GAA Glu	ATC Ile	AAA Lys	1082
CCC Pro	ACC Thr	TTC Phe	AGC Ser	CAG Gln	TTG Leu	GAA Glu	GCT Ala	GTC Val	AAC Asn	CTG Leu	CAT His	GAA Glu	GTC Val	AAA Lys	CAT His	1130
TTT Phe	GTT Val	GTA Val	GAG Glu	GTG Val	CGG Arg	GCC Ala	TAC Tyr	CCA Pro	CCT Pro	CCC Pro	AGG Arg	ATA Ile	TCC Ser	TGG Trp	CTG Leu	1178
AAA Lys	AAC Asn	AAT Asn	CTG Leu	ACT Thr	CTG Leu	ATT Ile	GAA Glu	AAT Asn	CTC Leu	ACT Thr	GAG Glu	ATC Ile	ACC Thr	ACT Thr	GAT Asp	1226
GTG Val	GAA Glu	AAG Lys	ATT Ile	CAG Gln	GAA Glu	ATA Ile	AGG Arg	TAT Tyr	CGA Arg	AGC Ser	AAA Lys	TTA Leu	AAG Lys	CTG Leu	ATC Ile	1274
CGT Arg	GCT Ala	AAG Lys	GAA Glu	GAA Glu	GAC Asp	AGT Ser	GGC Gly	CAT His	TAT Tyr	ACT Thr	ATT Ile	GTA Val	GCT Ala	CAA Gln	AAT Asn	1322
GAA Glu	GAT Asp	GCT Ala	GTG Val	AAG Lys	AGC Ser	TAT Tyr	ACT Thr	TTT Phe	GAA Glu	CTG Leu	TTA Leu	ACT Thr	CAA Gln	GTT Val	CCT Pro	1370
TCA Ser	TCC Ser	ATT Ile	CTG Leu	GAC Asp	TTG Leu	GTC Val	GAT Asp	GAT Asp	CAC His	CAT His	GGC Gly	TCA Ser	ACT Thr	GGG Gly	GGA Gly	1418
CAG Gln	ACG Thr	GTG Val	AGG Arg	TGC Cys	ACA Thr	GCT Ala	GAA Glu	GGC Gly	ACG Thr	CCG Pro	CTT Leu	CCT Pro	GAT Asp	ATT Ile	GAG Glu	1466
TGG Trp	ATG Met	ATA Ile	TGC Cys	AAA Lys	GAT Asp	ATT Ile	AAG Lys	AAA Lys	TGT Cys	AAT Asn	AAT Asn	GAA Glu	ACT Thr	TCC Ser	TGG Trp	1514
ACT Thr	ATT Ile	TTG Leu	GCC Ala	AAC Asn	AAT Asn	GTC Val	TCA Ser	AAC Asn	ATC Ile	ATC Ile	ACG Thr	GAG Glu	ATC Ile	CAC His	TCC Ser	1562
CGA Arg	GAC Asp	AGG Arg	AGT Ser	ACC Thr	GTG Val	GAG Glu	GGC Gly	CGT Arg	GTG Val	ACT Thr	TTC Phe	GCC Ala	AAA Lys	GTG Val	GAG Glu	1610
GAG Glu	ACC Thr	ATC Ile	GCC Ala	GTG Val	CGA Arg	TGC Cys	CTG Leu	GCT Ala	AAG Lys	AAT Asn	CTC Leu	CTT Leu	GGA Gly	GCT Ala	GAG Glu	1658
AAC Asn	CGA Arg	GAG Glu	CTG Leu	AAG Lys	CTG Leu	GTG Val	GCT Ala	CCC Pro	ACC Thr	CTG Leu	CGT Arg	TCT Ser	GAA Glu	CTC Leu	ACG Thr	1706

GTG	GCT	GCT	GCA	GTC	CTG	GTG	CTG	TTG	GTG	ATT	GTG	ATC	ATC	TCA	CTT	1754
Val	Ala	Ala	Ala	Val	Leu	Val	Leu	Leu	Val	Ile	Val	Ile	Ile	Ser	Leu	
			530					535					540			
ATT	GTC	CTG	GTT	GTC	ATT	TGG	AAA	CAG	AAA	CCG	AGG	TAT	GAA	ATT	CGC	1802
Ile	Val	Leu	Val	Val	Ile	Trp	Lys	Gln	Lys	Pro	Arg	Tyr	Glu	Ile	Arg	
		545					550					555				
TGG	AGG	GTC	ATT	GAA	TCA	ATC	AGC	CCA	GAT	GGA	CAT	GAA	TAT	ATT	TAT	1850
Trp	Arg	Val	Ile	Glu	Ser	Ile	Ser	Pro	Asp	Gly	His	Glu	Tyr	Ile	Tyr	
	560					565					570					
GTG	GAC	CCG	ATG	CAG	CTG	CCT	TAT	GAC	TCA	AGA	TGG	GAG	TTT	CCA	AGA	1898
Val	Asp	Pro	Met	Gln	Leu	Pro	Tyr	Asp	Ser	Arg	Trp	Glu	Phe	Pro	Arg	
	575				580					585					590	
GAT	GGA	CTA	GTG	CTT	GGT	CGG	GTC	TTG	GGG	TCT	GGA	GCG	TTT	GGG	AAG	1946
Asp	Gly	Leu	Val	Leu	Gly	Arg	Val	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Lys	
				595					600					605		
GTG	GTT	GAA	GGA	ACA	GCC	TAT	GGA	TTA	AGC	CGG	TCC	CAA	CCT	GTC	ATG	1994
Val	Val	Glu	Gly	Thr	Ala	Tyr	Gly	Leu	Ser	Arg	Ser	Gln	Pro	Val	Met	
			610					615					620			
AAA	GTT	GCA	GTG	AAG	ATG	CTA	AAA	CCC	ACG	GCC	AGA	TCC	AGT	GAA	AAA	2042
Lys	Val	Ala	Val	Lys	Met	Leu	Lys	Pro	Thr	Ala	Arg	Ser	Ser	Glu	Lys	
		625					630					635				
CAA	GCT	CTC	ATG	TCT	GAA	CTG	AAG	ATA	ATG	ACT	CAC	CTG	GGG	CCA	CAT	2090
Gln	Ala	Leu	Met	Ser	Glu	Leu	Lys	Ile	Met	Thr	His	Leu	Gly	Pro	His	
	640					645					650					
TTG	AAC	ATT	GTA	AAC	TTG	CTG	GGA	GCC	TGC	ACC	AAG	TCA	GGC	CCC	ATT	2138
Leu	Asn	Ile	Val	Asn	Leu	Leu	Gly	Ala	Cys	Thr	Lys	Ser	Gly	Pro	Ile	
	655				660					665					670	
TAC	ATC	ATC	ACA	GAG	TAT	TGC	TTC	TAT	GGA	GAT	TTG	GTC	AAC	TAT	TTG	2186
Tyr	Ile	Ile	Thr	Glu	Tyr	Cys	Phe	Tyr	Gly	Asp	Leu	Val	Asn	Tyr	Leu	
				675					680					685		
CAT	AAG	AAT	AGG	GAT	AGC	TTC	CTG	AGC	CAC	CAC	CCA	GAG	AAG	CCA	AAG	2234
His	Lys	Asn	Arg	Asp	Ser	Phe	Leu	Ser	His	His	Pro	Glu	Lys	Pro	Lys	
			690					695					700			
AAA	GAG	CTG	GAT	ATC	TTT	GGA	TTG	AAC	CCT	GCT	GAT	GAA	AGC	ACA	CGG	2282
Lys	Glu	Leu	Asp	Ile	Phe	Gly	Leu	Asn	Pro	Ala	Asp	Glu	Ser	Thr	Arg	
		705					710					715				
AGC	TAT	GTT	ATT	TTA	TCT	TTT	GAA	AAC	AAT	GGT	GAC	TAC	ATG	GAC	ATG	2330
Ser	Tyr	Val	Ile	Leu	Ser	Phe	Glu	Asn	Asn	Gly	Asp	Tyr	Met	Asp	Met	
	720					725					730					
AAG	CAG	GCT	GAT	ACT	ACA	CAG	TAT	GTC	CCC	ATG	CTA	GAA	AGG	AAA	GAG	2378
Lys	Gln	Ala	Asp	Thr	Thr	Gln	Tyr	Val	Pro	Met	Leu	Glu	Arg	Lys	Glu	
	735				740				745						750	
GTT	TCT	AAA	TAT	TCC	GAC	ATC	CAG	AGA	TCA	CTC	TAT	GAT	CGT	CCA	GCC	2426
Val	Ser	Lys	Tyr	Ser	Asp	Ile	Gln	Arg	Ser	Leu	Tyr	Asp	Arg	Pro	Ala	
				755					760					765		
TCA	TAT	AAG	AAG	AAA	TCT	ATG	TTA	GAC	TCA	GAA	GTC	AAA	AAC	CTC	CTT	2474
Ser	Tyr	Lys	Lys	Lys	Ser	Met	Leu	Asp	Ser	Glu	Val	Lys	Asn	Leu	Leu	
			770					775					780			
TCA	GAT	GAT	AAC	TCA	GAA	GGC	CTT	ACT	TTA	TTG	GAT	TTG	TTG	AGC	TTC	2522
Ser	Asp	Asp	Asn	Ser	Glu	Gly	Leu	Thr	Leu	Leu	Asp	Leu	Leu	Ser	Phe	
		785					790					795				

ACC	TAT	CAA	GTT	GCC	CGA	GGA	ATG	GAG	TTT	TTG	GCT	TCA	AAA	AAT	TGT	2570
Thr	Tyr	Gln	Val	Ala	Arg	Gly	Met	Glu	Phe	Leu	Ala	Ser	Lys	Asn	Cys	
800						805					810					
GTC	CAC	CGT	GAT	CTG	GCT	GCT	CGC	AAC	GTT	CTC	CTG	GCA	CAA	GGA	AAA	2618
Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Val	Leu	Leu	Ala	Gln	Gly	Lys	
815					820					825					830	
ATT	GTG	AAG	ATC	TGT	GAC	TTT	GGC	CTG	GCC	AGA	GAC	ATC	ATG	CAT	GAT	2666
Ile	Val	Lys	Ile	Cys	Asp	Phe	Gly	Leu	Ala	Arg	Asp	Ile	Met	His	Asp	
				835					840					845		
TCG	AAC	TAT	GTG	TCG	AAA	GGC	AGT	ACC	TTT	CTG	CCC	GTG	AAG	TGG	ATG	2714
Ser	Asn	Tyr	Val	Ser	Lys	Gly	Ser	Thr	Phe	Leu	Pro	Val	Lys	Trp	Met	
			850					855					860			
GCT	CCT	GAG	AGC	ATC	TTT	GAC	AAC	CTC	TAC	ACC	ACA	CTG	AGT	GAT	GTC	2762
Ala	Pro	Glu	Ser	Ile	Phe	Asp	Asn	Leu	Tyr	Thr	Thr	Leu	Ser	Asp	Val	
		865					870					875				
TGG	TCT	TAT	GGC	ATT	CTG	CTC	TGG	GAG	ATC	TTT	TCC	CTT	GGT	GGC	ACC	2810
Trp	Ser	Tyr	Gly	Ile	Leu	Leu	Trp	Glu	Ile	Phe	Ser	Leu	Gly	Gly	Thr	
	880				885						890					
CCT	TAC	CCC	GGC	ATG	ATG	GTG	GAT	TCT	ACT	TTC	TAC	AAT	AAG	ATC	AAG	2858
Pro	Tyr	Pro	Gly	Met	Met	Val	Asp	Ser	Thr	Phe	Tyr	Asn	Lys	Ile	Lys	
895					900					905					910	
AGT	GGG	TAC	CGG	ATG	GCC	AAG	CCT	GAC	CAC	GCT	ACC	AGT	GAA	GTC	TAC	2906
Ser	Gly	Tyr	Arg	Met	Ala	Lys	Pro	Asp	His	Ala	Thr	Ser	Glu	Val	Tyr	
				915					920					925		
GAG	ATC	ATG	GTG	AAA	TGC	TGG	AAC	AGT	GAG	CCG	GAG	AAG	AGA	CCC	TCC	2954
Glu	Ile	Met	Val	Lys	Cys	Trp	Asn	Ser	Glu	Pro	Glu	Lys	Arg	Pro	Ser	
			930					935					940			
TTT	TAC	CAC	CTG	AGT	GAG	ATT	GTG	GAG	AAT	CTG	CTG	CCT	GGA	CAA	TAT	3002
Phe	Tyr	His	Leu	Ser	Glu	Ile	Val	Glu	Asn	Leu	Leu	Pro	Gly	Gln	Tyr	
		945					950					955				
AAA	AAG	AGT	TAT	GAA	AAA	ATT	CAC	CTG	GAC	TTC	CTG	AAG	AGT	GAC	CAT	3050
Lys	Lys	Ser	Tyr	Glu	Lys	Ile	His	Leu	Asp	Phe	Leu	Lys	Ser	Asp	His	
	960					965					970					
CCT	GCT	GTG	GCA	CGC	ATG	CGT	GTG	GAC	TCA	GAC	AAT	GCA	TAC	ATT	GGT	3098
Pro	Ala	Val	Ala	Arg	Met	Arg	Val	Asp	Ser	Asp	Asn	Ala	Tyr	Ile	Gly	
975					980					985					990	
GTC	ACC	TAC	AAA	AAC	GAG	GAA	GAC	AAG	CTG	AAG	GAC	TGG	GAG	GGT	GGT	3146
Val	Thr	Tyr	Lys	Asn	Glu	Glu	Asp	Lys	Leu	Lys	Asp	Trp	Glu	Gly	Gly	
				995					1000					1005		
CTG	GAT	GAG	CAG	AGA	CTG	AGC	GCT	GAC	AGT	GGC	TAC	ATC	ATT	CCT	CTG	3194
Leu	Asp	Glu	Gln	Arg	Leu	Ser	Ala	Asp	Ser	Gly	Tyr	Ile	Ile	Pro	Leu	
			1010					1015					1020			
CCT	GAC	ATT	GAC	CCT	GTG	CCT	GAG	GAG	GAG	GAC	CTG	GGC	AAG	AGG	AAC	3242
Pro	Asp	Ile	Asp	Pro	Val	Pro	Glu	Glu	Glu	Asp	Leu	Gly	Lys	Arg	Asn	
		1025					1030					1035				
AGA	CAC	AGC	TCG	CAG	ACC	TCT	GAA	GAG	AGT	GCC	ATT	GAG	ACG	GGT	TCC	3290
Arg	His	Ser	Ser	Gln	Thr	Ser	Glu	Glu	Ser	Ala	Ile	Glu	Thr	Gly	Ser	
	1040					1045					1050					
AGC	AGT	TCC	ACC	TTC	ATC	AAG	AGA	GAG	GAC	GAG	ACC	ATT	GAA	GAC	ATC	3338
Ser	Ser	Ser	Thr	Phe	Ile	Lys	Arg	Glu	Asp	Glu	Thr	Ile	Glu	Asp	Ile	
1055					1060					1065					1070	

GAC ATG ATG GAC GAC ATC GGC ATA GAC TCT TCA GAC CTG GTG GAA GAC	3386
Asp Met Met Asp Asp Ile Gly Ile Asp Ser Ser Asp Leu Val Glu Asp	
1075 1080 1085	
AGC TTC CTG TAA CTGGCGGATT CGAGGGGTTT CTTCCACTTC TGGGGCCACC	3438
Ser Phe Leu *	
1090	
TCTGGATCCC GTTCAGAAAA CCACTTTTATT GCAATGCGGA GGTTGAGAGG AGGACTTGGT	3498
TGATGTTTAA AGAGAAGTTC CCAGCCAAGG GCCTCGGGGA GCCTTTCTAA ATATGAATGA	3558
ATGGGATATT TTGAAATGAA CTTTGTCTAGT GTTGCCCTCTT GCAATGCCTC AGTAGCATCT	3618
CAGTGGTGTG TGAAGTTTGG AGATAGATGG ATAAGGGAAT AATAGGCCAC AGAAGGTGAA	3678
CTTTCTGCTT CAAGGACATT GGTGAGAGTC CAACAGACAC AATTTATACT GCGACAGAAC	3738
TTCAGCATTG TAATTATGTA AATAACTCTA ACCACGGCTG TGTTTAGATT GTATTAACTA	3798
TCTTCTTTGG ACTTCTGAAG AGACCACTCA ATCCATCCAT GTACTTCCCT CTTGAAACCT	3858
GATGTCAGCT GCTGTTGAAC TTTTAAAGA AGTGCATGAA AAACCATTTT TGACCTTAAA	3918
AGGTACTGGT ACTATAGCAT TTTGCTATCT TTTTGTAGTGT TAAAGAGATA AAGAATAATA	3978
ATTAACCAAC CTTGTTTAAT AGATTTGGGT CATTTAGAAG CCTGACAACT CATTTTCATA	4038
TTGTAATCTA TGTTTATAAT ACTACTACTG TTATCAGTAA TGCTAAATGT GTAATAATGT	4098
AACATGATTT CCCTCCACAC AAAGCACAAT TTAAAAACAA TCCTTACTAA GTAGGTGATG	4158
AGTTTGACAG TTTTGTGACAT TTATATTAAA TAACATGTTT CTCTATAAAG TATGGTAATA	4218
GCTTTAGTGA ATTAAATTTA GTTGAGCATA GAGAACAAAG TAAAAGTAGT GTTGTCAGG	4278
AAGTCAGAAT TTTTAACTGT ACTGAATAGG TTCCCCAATC CATCGTATTA AAAAACAATT	4338
AACTGCCCTC TGAAATAATG GGATTAGAAA CAAACAAAAC TCTTAAGTCC TAAAAGTTCT	4398
CAATGTAGAG GCATAAACCT GTGCTGAACA TAACTTCTCA TGTATATTAC CCAATGGAAA	4458
ATATAATGAT CAGCGCAAAA GACTGGATTT GCAGAAGTTT TTTTTTTTTT TCTTCTTGCC	4518
TGATGAAAGC TTTGGCGACC CCAATATATG TATTTTTTGA ATCTATGAAC CTGAAAAGGG	4578
TCACAAAGGA TGCCAGACA TCAGCCTCCT TCTTTCACCC CTTACCCCAA AGAGAAAGAG	4638
TTTGAAACTC GAGACCATAA AGATATTCTT TAGTGGAGGC TGGAAGTGCA TTAGCCTGAT	4698
CCTCAGTTCT CAAATGTGTG TGGCAGCCAG GTAGACTAGT ACCTGGGTTT CCATCCTTGA	4758
GATTCTGAAG TATGAAGTCT GAGGGAAACC AGAGTCTGTA TTTTCTAAA CTCCCTGGCT	4818
GTTCTGATCG GCCAGGTTT GGAACACTG ACTTAGGTTT CAGGAAGTTG CCATGGGAAA	4878
CAAATAATTT GAACTTTGGA ACAGGGTTCT TAAGTTGGTG CGTCCTTCGG ATGATAAATT	4938
TAGGAACCGA AGTCCAATCA CTGTAAATTA CGGTAGATCG ATCGTTAACG CTGGAATTAA	4998
ATTGAAAGGT CAGAATCGAC TCCGACTCTT TCGATTTCAA ACCAAAAGT TCCAAAAGGT	5058
TTTCATTTCT ACGATGAAGG GTGACATACC CCCTCTAACT TGAAAGGGGC AGAGGGCAGA	5118
AGAGCGGAGG GTGAGGTATG GGGCGGTTCC TTTCCGTACA TGTTTTTAAT ACGTTAAGTC	5178
ACAAGGTTCA GAGACACATT GGTGAGTCA CAAAACCACC TTTTTTGTA AATTCAAAAT	5238

GACTATTAAA CTCCAATCTA CCCTCCTACT TAACAGTGTA GATAGGTGTG ACAGTTTGTC	5298
CAACCACACC CAAGTAACCG TAAGAAACGT TATGACGAAT TAACGACTAT GGTATACTTA	5358
CTTTGTACCC GACACTAATG ACGTTAGTGA CACGATAGCC GTCTACTACG AAACCTTCTA	5418
CGTCTTCGTT ATTATTTTCAT GAACTGATGG ATGACCACAT TAGAGTTACG TTCGGGGTTG	5478
AAAGAATAGG TTGAAAAAGT ATCATTACAG CTTCTGACTC GGTCTAACCG GTTAATTTTT	5538
CTTTTGACT GATCCAAGAC ATCTCGGTTA ATCTGAACCTT TATGCAAACA CAAAGATCTT	5598
AGTGTCGAGT TCGTAAGACA AATAGCGAGT GAGAGGGAAC ATGTCGGAAT AAAACAACCA	5658
CGAAACGTAA AACTATAACG AACTCGGAA CGTACTGTAG TACTCCGGCC TACTTTGAAG	5718
AGTCAGGTCG TCAAAGGTCA GGATTGTTTA CGAGGGTGGA CTTAAACATA TACTGACGTA	5778
AACACCCACA CACACACAAA AGTCGTTTAA GGTCTAAACA AAGGAAAACC GGAGGACGTT	5838
TCAGAGGTCT TCTTTTAAAC GGTTAGAAAAG GATGAAAGAT AAAAATACTA CTGTTAGTTT	5898
CGGCCGGACT CTTTGTGATA AACACTGAAA AATTTGCTAA TCACTACAGG AATTTTACAC	5958
CAGACGGTTA GACATGTTTT ACCAGGATAA AAACACTTCT CCCTGTATTTC TATTTTACTA	6018
CAATATGTAG TTATACATAT ATACATAAAG ATATATCTGA ACCTCTTATG ACGGTTTTGT	6078
AAATACTGTT CGACATAGTG ACGGAAGCAA ATATAAAAAA ATTGACACTA TTAGGGGTGT	6138
CCGTGTAATT GACAACGTGA AAACCTACAG GTTTTAAATA TAAATCTTT ATTATTTTTC	6198
TTTCTATGAA TGTACAAGGG TTTTGTACC ACACCACTTA CACACTCTTT TTGATTGAAC	6258
TATCCCAGAT GGTTATGTTT TACATAATGC TTACGGGGAC AAGTACAAAA ACAAAATTTT	6318
GCACATTTAC TTCTAGAAAT ATAAAGTTAT TTAATTTCC TTAAG	6373

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1090 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Gly	Thr	Ser	His	Pro	Ala	Phe	Leu	Val	Leu	Gly	Cys	Leu	Leu	Thr
1				5					10					15	
Gly	Leu	Ser	Leu	Ile	Leu	Cys	Gln	Leu	Ser	Leu	Pro	Ser	Ile	Leu	Pro
			20					25					30		
Asn	Glu	Asn	Glu	Lys	Val	Val	Gln	Leu	Asn	Ser	Ser	Phe	Ser	Leu	Arg
			35					40					45		
Cys	Phe	Gly	Glu	Ser	Glu	Val	Ser	Trp	Gln	Tyr	Pro	Met	Ser	Glu	Glu
			50				55				60				
Glu	Ser	Ser	Asp	Val	Glu	Ile	Arg	Asn	Glu	Glu	Asn	Asn	Ser	Gly	L u
			65			70			75						80
Phe	Val	Thr	Val	Leu	Glu	Val	Ser	Ser	Ala	Ser	Ala	Ala	His	Thr	Gly
				85					90						95

Leu Tyr Thr Cys Tyr Tyr Asn His Thr Gln Thr Glu Glu Asn Glu Leu
 100 105 110
 Glu Gly Arg His Ile Tyr Ile Tyr Val Pro Asp Pro Asp Val Ala Phe
 115 120 125
 Val Pro Leu Gly Met Thr Asp Tyr Leu Val Ile Val Glu Asp Asp Asp
 130 135 140
 Ser Ala Ile Ile Pro Cys Arg Thr Thr Asp Pro Glu Thr Pro Val Thr
 145 150 155 160
 Leu His Asn Ser Glu Gly Val Val Pro Ala Ser Tyr Asp Ser Arg Gln
 165 170 175
 Gly Phe Asn Gly Thr Phe Thr Val Gly Pro Tyr Ile Cys Glu Ala Thr
 180 185 190
 Val Lys Gly Lys Lys Phe Gln Thr Ile Pro Phe Asn Val Tyr Ala Leu
 195 200 205
 Lys Ala Thr Ser Glu Leu Asp Leu Glu Met Glu Ala Leu Lys Thr Val
 210 215 220
 Tyr Lys Ser Gly Glu Thr Ile Val Val Thr Cys Ala Val Phe Asn Asn
 225 230 235 240
 Glu Val Val Asp Leu Gln Trp Thr Tyr Pro Gly Glu Val Lys Gly Lys
 245 250 255
 Gly Ile Thr Met Leu Glu Glu Ile Lys Val Pro Ser Ile Lys Leu Val
 260 265 270
 Tyr Thr Leu Thr Val Pro Glu Ala Thr Val Lys Asp Ser Gly Asp Tyr
 275 280 285
 Glu Cys Ala Ala Arg Gln Ala Thr Arg Glu Val Lys Glu Met Lys Lys
 290 295 300
 Val Thr Ile Ser Val His Glu Lys Gly Phe Ile Glu Ile Lys Pro Thr
 305 310 315 320
 Phe Ser Gln Leu Glu Ala Val Asn Leu His Glu Val Lys His Phe Val
 325 330 335
 Val Glu Val Arg Ala Tyr Pro Pro Pro Arg Ile Ser Trp Leu Lys Asn
 340 345 350
 Asn Leu Thr Leu Ile Glu Asn Leu Thr Glu Ile Thr Thr Asp Val Glu
 355 360 365
 Lys Ile Gln Glu Ile Arg Tyr Arg Ser Lys Leu Lys Leu Ile Arg Ala
 370 375 380
 Lys Glu Glu Asp Ser Gly His Tyr Thr Ile Val Ala Gln Asn Glu Asp
 385 390 395 400
 Ala Val Lys Ser Tyr Thr Phe Glu Leu Leu Thr Gln Val Pro Ser Ser
 405 410 415
 Ile Leu Asp Leu Val Asp Asp His His Gly Ser Thr Gly Gly Gln Thr
 420 425 430
 Val Arg Cys Thr Ala Glu Gly Thr Pro Leu Pro Asp Ile Glu Trp Met
 435 440 445

Ile	Cys	Lys	Asp	Ile	Lys	Lys	Cys	Asn	Asn	Glu	Thr	Ser	Trp	Thr	Ile
450						455					460				
Leu	Ala	Asn	Asn	Val	Ser	Asn	Ile	Ile	Thr	Glu	Ile	His	Ser	Arg	Asp
465					470					475					480
Arg	Ser	Thr	Val	Glu	Gly	Arg	Val	Thr	Phe	Ala	Lys	Val	Glu	Glu	Thr
				485					490					495	
Ile	Ala	Val	Arg	Cys	Leu	Ala	Lys	Asn	Leu	Leu	Gly	Ala	Glu	Asn	Arg
			500					505					510		
Glu	Leu	Lys	Leu	Val	Ala	Pro	Thr	Leu	Arg	Ser	Glu	Leu	Thr	Val	Ala
		515					520					525			
Ala	Ala	Val	Leu	Val	Leu	Leu	Val	Ile	Val	Ile	Ile	Ser	Leu	Ile	Val
	530					535					540				
Leu	Val	Val	Ile	Trp	Lys	Gln	Lys	Pro	Arg	Tyr	Glu	Ile	Arg	Trp	Arg
545					550					555					560
Val	Ile	Glu	Ser	Ile	Ser	Pro	Asp	Gly	His	Glu	Tyr	Ile	Tyr	Val	Asp
				565					570					575	
Pro	Met	Gln	Leu	Pro	Tyr	Asp	Ser	Arg	Trp	Glu	Phe	Pro	Arg	Asp	Gly
			580					585					590		
Leu	Val	Leu	Gly	Arg	Val	Leu	Gly	Ser	Gly	Ala	Phe	Gly	Lys	Val	Val
		595					600					605			
Glu	Gly	Thr	Ala	Tyr	Gly	Leu	Ser	Arg	Ser	Gln	Pro	Val	Met	Lys	Val
	610					615					620				
Ala	Val	Lys	Met	Leu	Lys	Pro	Thr	Ala	Arg	Ser	Ser	Glu	Lys	Gln	Ala
625					630					635					640
Leu	Met	Ser	Glu	Leu	Lys	Ile	Met	Thr	His	Leu	Gly	Pro	His	Leu	Asn
				645					650					655	
Ile	Val	Asn	Leu	Leu	Gly	Ala	Cys	Thr	Lys	Ser	Gly	Pro	Ile	Tyr	Ile
			660					665					670		
Ile	Thr	Glu	Tyr	Cys	Phe	Tyr	Gly	Asp	Leu	Val	Asn	Tyr	Leu	His	Lys
		675					680					685			
Asn	Arg	Asp	Ser	Phe	Leu	Ser	His	His	Pro	Glu	Lys	Pro	Lys	Lys	Glu
	690					695					700				
Leu	Asp	Ile	Phe	Gly	Leu	Asn	Pro	Ala	Asp	Glu	Ser	Thr	Arg	Ser	Tyr
705					710					715					720
Val	Ile	Leu	Ser	Phe	Glu	Asn	Asn	Gly	Asp	Tyr	Met	Asp	Met	Lys	Gln
				725					730					735	
Ala	Asp	Thr	Thr	Gln	Tyr	Val	Pro	Met	Leu	Glu	Arg	Lys	Glu	Val	Ser
			740					745					750		
Lys	Tyr	Ser	Asp	Ile	Gln	Arg	Ser	Leu	Tyr	Asp	Arg	Pro	Ala	Ser	Tyr
		755					760					765			
Lys	Lys	Lys	Ser	Met	Leu	Asp	Ser	Glu	Val	Lys	Asn	Leu	Leu	Ser	Asp
	770					775					780				
Asp	Asn	Ser	Glu	Gly	Leu	Thr	Leu	Leu	Asp	Leu	Leu	Ser	Ph	Thr	Tyr
785					790					795					800

Gln Val Ala Arg Gly Met Glu Phe Leu Ala Ser Lys Asn Cys Val His
 805 810 815
 Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Ala Gln Gly Lys Ile Val
 820 825 830
 Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Met His Asp Ser Asn
 835 840 845
 Tyr Val Ser Lys Gly Ser Thr Phe Leu Pro Val Lys Trp Met Ala Pro
 850 855 860
 Glu Ser Ile Phe Asp Asn Leu Tyr Thr Thr Leu Ser Asp Val Trp Ser
 865 870 875 880
 Tyr Gly Ile Leu Leu Trp Glu Ile Phe Ser Leu Gly Gly Thr Pro Tyr
 885 890 895
 Pro Gly Met Met Val Asp Ser Thr Phe Tyr Asn Lys Ile Lys Ser Gly
 900 905 910
 Tyr Arg Met Ala Lys Pro Asp His Ala Thr Ser Glu Val Tyr Glu Ile
 915 920 925
 Met Val Lys Cys Trp Asn Ser Glu Pro Glu Lys Arg Pro Ser Phe Tyr
 930 935 940
 His Leu Ser Glu Ile Val Glu Asn Leu Leu Pro Gly Gln Tyr Lys Lys
 945 950 955 960
 Ser Tyr Glu Lys Ile His Leu Asp Phe Leu Lys Ser Asp His Pro Ala
 965 970 975
 Val Ala Arg Met Arg Val Asp Ser Asp Asn Ala Tyr Ile Gly Val Thr
 980 985 990
 Tyr Lys Asn Glu Glu Asp Lys Leu Lys Asp Trp Glu Gly Gly Leu Asp
 995 1000 1005
 Glu Gln Arg Leu Ser Ala Asp Ser Gly Tyr Ile Ile Pro Leu Pro Asp
 1010 1015 1020
 Ile Asp Pro Val Pro Glu Glu Glu Asp Leu Gly Lys Arg Asn Arg His
 1025 1030 1035 1040
 Ser Ser Gln Thr Ser Glu Glu Ser Ala Ile Glu Thr Gly Ser Ser Ser
 1045 1050 1055
 Ser Thr Phe Ile Lys Arg Glu Asp Glu Thr Ile Glu Asp Ile Asp Met
 1060 1065 1070
 Met Asp Asp Ile Gly Ile Asp Ser Ser Asp Leu Val Glu Asp Ser Phe
 1075 1080 1085
 Leu *
 1090

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5427 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 187..3507

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGTTCTCCTG AGCCTTCAGG AGCCTGCACC AGTCCTGCCT GTCCTTCTAC TCAGCTGTTA	60
CCCACCTCTGG GACCAGCAGT CTTTCTGATA ACTGGGAGAG GGCAGTAAGG AGGACTTCCT	120
GGAGGGGGGTG ACTGTCCAGA GCCTGGAACCT GTGCCACAC CAGAAGCCAT CAGCAGCAAG	180
GACACC ATG CGG CTT CCG GGT GCG ATG CCA GCT CTG GCC CTC AAA GGC	228
Met Arg Leu Pro Gly Ala Met Pro Ala Leu Ala Leu Lys Gly	
1095 1100	
GAG CTG CTG TTG CTG TCT CTC CTG TTA CTT CTG GAA CCA CAG ATC TCT	276
Glu Leu Leu Leu Leu Ser Leu Leu Leu Leu Leu Glu Pro Gln Ile Ser	
1105 1110 1115 1120	
CAG GGC CTG GTC GTC ACA CCC CCG GGG CCA GAG CTT GTC CTC AAT GTC	324
Gln Gly Leu Val Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn Val	
1125 1130 1135	
TCC AGC ACC TTC GTT CTG ACC TGC TCG GGT TCA GCT CCG GTG GTG TGG	372
Ser Ser Thr Phe Val Leu Thr Cys Ser Gly Ser Ala Pro Val Val Trp	
1140 1145 1150	
GAA CGG ATG TCC CAG GAG CCC CCA CAG GAA ATG GCC AAG GCC CAG GAT	420
Glu Arg Met Ser Gln Glu Pro Pro Gln Glu Met Ala Lys Ala Gln Asp	
1155 1160 1165	
GGC ACC TTC TCC AGC GTG CTC ACA CTG ACC AAC CTC ACT GGG CTA GAC	468
Gly Thr Phe Ser Ser Val Leu Thr Leu Thr Asn Leu Thr Gly Leu Asp	
1170 1175 1180	
ACG GGA GAA TAC TTT TGC ACC CAC AAT GAC TCC CGT GGA CTG GAG ACC	516
Thr Gly Glu Tyr Phe Cys Thr His Asn Asp Ser Arg Gly Leu Glu Thr	
1185 1190 1195 1200	
GAT GAG CGG AAA CGG CTC TAC ATC TTT GTG CCA GAT CCC ACC GTG GGC	564
Asp Glu Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp Pro Thr Val Gly	
1205 1210 1215	
TTC CTC CCT AAT GAT GCC GAG GAA CTA TTC ATC TTT CTC ACG GAA ATA	612
Phe Leu Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe Leu Thr Glu Ile	
1220 1225 1230	
ACT GAG ATC ACC ATT CCA TGC CGA GTA ACA GAC CCA CAG CTG GTG GTG	660
Thr Glu Ile Thr Ile Pro Cys Arg Val Thr Asp Pro Gln Leu Val Val	
1235 1240 1245	
ACA CTG CAC GAG AAG AAA GGG GAC GTT GCA CTG CCT GTC CCC TAT GAT	708
Thr Leu His Glu Lys Lys Gly Asp Val Ala Leu Pro Val Pro Tyr Asp	
1250 1255 1260	
CAC CAA CGT GGC TTT TCT GGT ATC TTT GAG GAC AGA AGC TAC ATC TGC	756
His Gln Arg Gly Phe Ser Gly Ile Phe Glu Asp Arg Ser Tyr Ile Cys	
1265 1270 1275 1280	
AAA ACC ACC ATT GGG GAC AGG GAG GTG GAT TCT GAT GCC TAC TAT GTC	804
Lys Thr Thr Ile Gly Asp Arg Glu Val Asp Ser Asp Ala Tyr Tyr Val	
1285 1290 1295	

TAC AGA CTC CAG GTG TCA TCC ATC AAC GTC TCT GTG AAC GCA GTG CAG Tyr Arg Leu Gln Val Ser Ser Ile Asn Val Ser Val Asn Ala Val Gln 1300 1305 1310	852
ACT GTG GTC CGC CAG GGT GAG AAC ATC ACC CTC ATG TGC ATT GTG ATC Thr Val Val Arg Gln Gly Glu Asn Ile Thr Leu Met Cys Ile Val Ile 1315 1320 1325	900
GGG AAT GAT GTG GTC AAC TTC GAG TGG ACA TAC CCC CGC AAA GAA AGT Gly Asn Asp Val Val Asn Phe Glu Trp Thr Tyr Pro Arg Lys Glu Ser 1330 1335 1340	948
GGG CGG CTG GTG GAG CCG GTG ACT GAC TTC CTC TTG GAT ATG CCT TAC Gly Arg Leu Val Glu Pro Val Thr Asp Phe Leu Leu Asp Met Pro Tyr 1345 1350 1355 1360	996
CAC ATC CGC TCC ATC CTG CAC ATC CCC AGT GCC GAG TTA GAA GAC TCG His Ile Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp Ser 1365 1370 1375	1044
GGG ACC TAC ACC TGC AAT GTG ACG GAG AGT GTG AAT GAC CAT CAG GAT Gly Thr Tyr Thr Cys Asn Val Thr Glu Ser Val Asn Asp His Gln Asp 1380 1385 1390	1092
GAA AAG GCC ATC AAC ATC ACC GTG GTT GAG AGC GGC TAC GTG CGG CTC Glu Lys Ala Ile Asn Ile Thr Val Val Glu Ser Gly Tyr Val Arg Leu 1395 1400 1405	1140
CTG GGA GAG GTG GGC ACA CTA CAA TTT GCT GAG CTG CAT CGG AGC CGG Leu Gly Glu Val Gly Thr Leu Gln Phe Ala Glu Leu His Arg Ser Arg 1410 1415 1420	1188
ACA CTG CAG GTA GTG TTC GAG GCC TAC CCA CCG CCC ACT GTC CTG TGG Thr Leu Gln Val Val Phe Glu Ala Tyr Pro Pro Pro Thr Val Leu Trp 1425 1430 1435 1440	1236
TTC AAA GAC AAC CGC ACC CTG GGC GAC TCC AGC GCT GGC GAA ATC GCC Phe Lys Asp Asn Arg Thr Leu Gly Asp Ser Ser Ala Gly Glu Ile Ala 1445 1450 1455	1284
CTG TCC ACG CGC AAC GTG TCG GAG ACC CGG TAT GTG TCA GAG CTG ACA Leu Ser Thr Arg Asn Val Ser Glu Thr Arg Tyr Val Ser Glu Leu Thr 1460 1465 1470	1332
CTG GTT CGC GTG AAG GTG GCA GAG GCT GGC CAC TAC ACC ATG CGG GCC Leu Val Arg Val Lys Val Ala Glu Ala Gly His Tyr Thr Met Arg Ala 1475 1480 1485	1380
TTC CAT GAG GAT GCT GAG GTC CAG CTC TCC TTC CAG CTA CAG ATC AAT Phe His Glu Asp Ala Glu Val Gln Leu Ser Phe Gln Leu Gln Ile Asn 1490 1495 1500	1428
GTC CCT GTC CGA GTG CTG GAG CTA AGT GAG AGC CAC CCT GAC AGT GGG Val Pro Val Arg Val Leu Glu Leu Ser Glu Ser His Pro Asp Ser Gly 1505 1510 1515 1520	1476
GAA CAG ACA GTC CGC TGT CGT GGC CGG GGC ATG CCG CAG CCG AAC ATC Glu Gln Thr Val Arg Cys Arg Gly Arg Gly Met Pro Gln Pro Asn Ile 1525 1530 1535	1524
ATC TGG TCT GCC TGC AGA GAC CTC AAA AGG TGT CCA CGT GAG CTG CCG Ile Trp Ser Ala Cys Arg Asp Leu Lys Arg Cys Pro Arg Glu Leu Pro 1540 1545 1550	1572
CCC ACG CTG CTG GGG AAC AGT TCC GAA GAG GAG AGC CAG CTG GAG ACT Pro Thr Leu Leu Gly Asn Ser Ser Glu Glu Glu Ser Gln Leu Glu Thr 1555 1560 1565	1620

AAC GTG ACG TAC TGG GAG GAG GAG CAG GAG TTT GAG GTG GTG AGC ACA Asn Val Thr Tyr Trp Glu Glu Glu Gln Glu Phe Glu Val Val Ser Thr 1570 1575 1580	1668
CTG CGT CTG CAG CAC GTG GAT CGG CCA CTG TCG GTG CGC TGC ACG CTG Leu Arg Leu Gln His Val Asp Arg Pro Leu Ser Val Arg Cys Thr Leu 1585 1590 1595 1600	1716
CGC AAC GCT GTG GGC CAG GAC ACG CAG GAG GTC ATC GTG GTG CCA CAC Arg Asn Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His 1605 1610 1615	1764
TCC TTG CCC TTT AAG GTG GTG GTG ATC TCA GCC ATC CTG GCC CTG GTG Ser Leu Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val 1620 1625 1630	1812
GTG CTC ACC ATC ATC TCC CTT ATC ATC CTC ATC ATG CTT TGG CAG AAG Val Leu Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys 1635 1640 1645	1860
AAG CCA CGT TAC GAG ATC CGA TGG AAG GTG ATT GAG TCT GTG AGC TCT Lys Pro Arg Tyr Glu Ile Arg Trp Lys Val Ile Glu Ser Val Ser Ser 1650 1655 1660	1908
GAC GGC CAT GAG TAC ATC TAC GTG GAC CCC ATG CAG CTG CCC TAT GAC Asp Gly His Glu Tyr Ile Tyr Val Asp Pro Met Gln Leu Pro Tyr Asp 1665 1670 1675 1680	1956
TCC ACG TGG GAG CTG CCG CGG GAC CAG CTT GTG CTG GGA CGC ACC CTC Ser Thr Trp Glu Leu Pro Arg Asp Gln Leu Val Leu Gly Arg Thr Leu 1685 1690 1695	2004
GGC TCT GGG GCC TTT GGG CAG GTG GTG GAG GCC ACA GCT CAT GGT CTG Gly Ser Gly Ala Phe Gly Gln Val Val Glu Ala Thr Ala His Gly Leu 1700 1705 1710	2052
AGC CAT TCT CAG GCC ACG ATG AAA GTG GCC GTC AAG ATG CTT AAA TCC Ser His Ser Gln Ala Thr Met Lys Val Ala Val Lys Met Leu Lys Ser 1715 1720 1725	2100
ACA GCC CGC AGC AGT GAG AAG CAA GCC CTT ATG TCG GAG CTG AAG ATC Thr Ala Arg Ser Ser Glu Lys Gln Ala Leu Met Ser Glu Leu Lys Ile 1730 1735 1740	2148
ATG AGT CAC CTT GGG CCC CAC CTG AAC GTG GTC AAC CTG TTG GGG GCC Met Ser His Leu Gly Pro His Leu Asn Val Val Asn Leu Leu Gly Ala 1745 1750 1755 1760	2196
TGC ACC AAA GGA GGA CCC ATC TAT ATC ATC ACT GAG TAC TGC CGC TAC Cys Thr Lys Gly Gly Pro Ile Tyr Ile Ile Thr Glu Tyr Cys Arg Tyr 1765 1770 1775	2244
GGA GAC CTG GTG GAC TAC CTG CAC CGC AAC AAA CAC ACC TTC CTG CAG Gly Asp Leu Val Asp Tyr Leu His Arg Asn Lys His Thr Phe Leu Gln 1780 1785 1790	2292
CAC CAC TCC GAC AAG CGC CGC CCG CCC AGC GCG GAG CTC TAC AGC AAT His His Ser Asp Lys Arg Arg Pro Pro Ser Ala Glu Leu Tyr Ser Asn 1795 1800 1805	2340
GCT CTG CCC GTT GGG CTC CCC CTG CCC AGC CAT GTG TCC TTG ACC GGG Ala Leu Pro Val Gly Leu Pro Leu Pro Ser His Val Ser Leu Thr Gly 1810 1815 1820	2388
GAG AGC GAC GGT GGC TAC ATG GAC ATG AGC AAG GAC GAG TCG GTG GAC Glu Ser Asp Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Val Asp 1825 1830 1835 1840	2436

TAT GTG CCC ATG CTG GAC ATG AAA GGA GAC GTC AAA TAT GCA GAC ATC Tyr Val Pro Met Leu Asp Met Lys Gly Asp Val Lys Tyr Ala Asp Ile 1845 1850 1855	2484
GAG TCC TCC AAC TAC ATG GCC CCT TAC GAT AAC TAC GTT CCC TCT GCC Glu Ser Ser Asn Tyr Met Ala Pro Tyr Asp Asn Tyr Val Pro Ser Ala 1860 1865 1870	2532
CCT GAG AGG ACC TGC CGA GCA ACT TTG ATC AAC GAG TCT CCA GTG CTA Pro Glu Arg Thr Cys Arg Ala Thr Leu Ile Asn Glu Ser Pro Val Leu 1875 1880 1885	2580
AGC TAC ATG GAC CTC GTG GGC TTC AGC TAC CAG GTG GCC AAT GGC ATG Ser Tyr Met Asp Leu Val Gly Phe Ser Tyr Gln Val Ala Asn Gly Met 1890 1895 1900	2628
GAG TTT CTG GCC TCC AAG AAC TGC GTC CAC AGA GAC CTG GCG GCT AGG Glu Phe Leu Ala Ser Lys Asn Cys Val His Arg Asp Leu Ala Ala Arg 1905 1910 1915 1920	2676
AAC GTG CTC ATC TGT GAA GGC AAG CTG GTC AAG ATC TGT GAC TTT GGC Asn Val Leu Ile Cys Glu Gly Lys Leu Val Lys Ile Cys Asp Phe Gly 1925 1930 1935	2724
CTG GCT CGA GAC ATC ATG CGG GAC TCG AAT TAC ATC TCC AAA GGC AGC Leu Ala Arg Asp Ile Met Arg Asp Ser Asn Tyr Ile Ser Lys Gly Ser 1940 1945 1950	2772
ACC TTT TTG CCT TTA AAG TGG ATG GCT CCG GAG AGC ATC TTC AAC AGC Thr Phe Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Ser 1955 1960 1965	2820
CTC TAC ACC ACC CTG AGC GAC GTG TGG TCC TTC GGG ATC CTG CTC TGG Leu Tyr Thr Thr Leu Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp 1970 1975 1980	2868
GAG ATC TTC ACC TTG GGT GGC ACC CCT TAC CCA GAG CTG CCC ATG AAC Glu Ile Phe Thr Leu Gly Gly Thr Pro Tyr Pro Glu Leu Pro Met Asn 1985 1990 1995 2000	2916
GAG CAG TTC TAC AAT GCC ATC AAA CGG GGT TAC CGC ATG GCC CAG CCT Glu Gln Phe Tyr Asn Ala Ile Lys Arg Gly Tyr Arg Met Ala Gln Pro 2005 2010 2015	2964
GCC CAT GCC TCC GAC GAG ATC TAT GAG ATC ATG CAG AAG TGC TGG GAA Ala His Ala Ser Asp Glu Ile Tyr Glu Ile Met Gln Lys Cys Trp Glu 2020 2025 2030	3012
GAG AAG TTT GAG ATT CGG CCC CCC TTC TCC CAG CTG GTG CTG CTT CTC Glu Lys Phe Glu Ile Arg Pro Pro Phe Ser Gln Leu Val Leu Leu Leu 2035 2040 2045	3060
GAG AGA CTG TTG GGC GAA GGT TAC AAA AAG AAG TAC CAG CAG GTG GAT Glu Arg Leu Leu Gly Glu Tyr Lys Lys Lys Tyr Gln Gln Val Asp 2050 2055 2060	3108
GAG GAG TTT CTG AGG AGT GAC CAC CCA GCC ATC CTT CGG TCC CAG GCC Glu Glu Phe Leu Arg Ser Asp His Pro Ala Ile Leu Arg Ser Gln Ala 2065 2070 2075 2080	3156
CGC TTG CCT GGG TTC CAT GGC CTC CGA TCT CCC CTG GAC ACC AGC TCC Arg Leu Pro Gly Phe His Gly Leu Arg Ser Pro Leu Asp Thr Ser Ser 2085 2090 2095	3204
GTC CTC TAT ACT GCC GTG CAG CCC AAT GAG GGT GAC AAC GAC TAT ATC Val Leu Tyr Thr Ala Val Gln Pro Asn Glu Gly Asp Asn Asp Tyr Ile 2100 2105 2110	3252

ATC CCC CTG CCT GAC CCC AAA CCT GAG GTT GCT GAC GAG GGC CCA CTG Ile Pro Leu Pro Asp Pro Lys Pro Glu Val Ala Asp Glu Gly Pro Leu 2115 2120 2125	3300
GAG GGT TCC CCC AGC CTA GCC AGC TCC ACC CTG AAT GAA GTC AAC ACC Glu Gly Ser Pro Ser Leu Ala Ser Ser Thr Leu Asn Glu Val Asn Thr 2130 2135 2140	3348
TCC TCA ACC ATC TCC TGT GAC AGC CCC CTG GAG CCC CAG GAC GAA CCA Ser Ser Thr Ile Ser Cys Asp Ser Pro Leu Glu Pro Gln Asp Glu Pro 2145 2150 2155 2160	3396
GAG CCA GAG CCC CAG CTT GAG CTC CAG GTG GAG CCG GAG CCG GAG CTG Glu Pro Glu Pro Gln Leu Glu Leu Gln Val Glu Pro Glu Pro Glu Leu 2165 2170 2175	3444
GAA CAG TTG CCG GAT TCG GGG TGC CCT GCG CCT CGG GCG GAA GCA GAG Glu Gln Leu Pro Asp Ser Gly Cys Pro Ala Pro Arg Ala Glu Ala Glu 2180 2185 2190	3492
GAT AGC TTC CTG TAG GGGGCTGGCC CCTACCCTGC CCTGCCTGAA GCTCCCCCGC Asp Ser Phe Leu * 2195	3547
TGCCAGCACC CAGCATCTCC TGGCCTGGCC TGGCCGGGCT TCCTGTCAGC CAGGCTGCCC	3607
TTATCAGCTG TCCCCTTCTG GAAGCTTTCT GCTCCTGACG TGTGTGCCCC CAAACCCTGG	3667
GGCTGGCTTA GGAGGCAAGA AAAGTGCAGG GGCCGTGACC AGCCCTCTGC CTCCAGGGAG	3727
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GAAAGTTAGG CTGTATGACC CAGAATCTAG GATTCTCTCC CTGGCTGACA GGTGGGGAGA	3847
CCGAATCCCT CCCTGGGAAG ATTCTTGGAG TTAGTGAGGT GGTAAATTAA CTTTTTTCTG	3907
TTCAGCCAGC TACCCCTCAA GGAATCATAG CTCTCTCCTC GCACTTTTAT CCACCCAGGA	3967
GCTAGGGAAG AGACCCTAGC CTCCTGGCT GCTGGCTGAG CTAGGGCCTA GCCTTGAGCA	4027
GTGTTGCCTC ATCCAGAAGA AAGCCAGTCT CCTCCCTATG ATGCCAGTCC CTGCGTTCCC	4087
TGGCCCGAGC TGGTCTGGGG CCATTAGGCA GCCTAATTAA TGCTGGAGGC TGAGCCAAGT	4147
ACAGGACACC CCCAGCCTGC AGCCCTTGCC CAGGGCACTT GGAGCACACG CAGCCATAGC	4207
AAGTGCCTGT GTCCCTGTCC TTCAGGCCCA TCAGTCCTGG GGCTTTTTCT TTATCACCTT	4267
CAGTCTTAAT CCATCCACCA GAGTCTAGAA GGCCAGACGG GCCCCGCATC TGTGATGAGA	4327
ATGTAAATGT GCCAGTGTGG AGTGGCCACG TGTGTGTGCC AGATATGGCC CTGGCTCTGC	4387
ATTGGACCTG CTATGAGGCT TTGGAGGAAT CCCTCACCTT CTCTGGGCCT CAGTTTCCCC	4447
TTCAAAAAAT GAATAAGTCG GACTTATTAA CTCTGAGTGC CTTGCCAGCA CTAACATTCT	4507
AGAGTATCCA GGTGGTTGCA CATTTGTCCA GATGAAGCAA GGCCATATAC CCTAAACTTC	4567
CATCCTGGGG GTCAGCTGGG CTCCTGGGAG ATTCCAGATC ACACATCACA CTCTGGGGAC	4627
TCAGGAACCA TGCCCTTCC CCAGGCCCCC AGCAAGTCTC AAGAACACAG CTGCACAGGC	4687
CTTGACTTAG AGTGACAGCC GGTGTCCTGG AAAGCCCCCA GCAGCTGCCC CAGGGACATG	4747
GGAAGACCAC GGGACCTCTT TCACTACCCA CGATGACCTC CGGGGGTATC CTGGGCAAAA	4807
GGGACAAAGA GGGCAAATGA GATCACCTCC TGCAGCCAC CACTCCAGCA CCTGTGCCGA	4867

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GGTCTGCGTC GAAGACAGAA TGGACAGTGA GGACAGTTAT GTCTTGTAAG AGACAAGAAG 4927
CTTCAGATGG GTACCCCAAG AAGGATGTGA GAGGTGGGCG CTTTGGAGGT TTGCCCCTCA 4987
CCCACCAGCT GCCCCATCCC TGAGGCAGCG CTCCATGGGG GTATGGTTTT GTCAGTCCCC 5047
AGACCTAGCA GTGACATCTC ATTGTCCCCA GCCCAGTGGG CATTGGAGGT GCCAGGGGAG 5107
TCAGGGTTGT AGCCAAGACG CCCCCGCACG GGGAGGGTTG GGAAGGGGGT GCAGGAAGCT 5167
CAACCCCTCT GGGCACCAAC CCTGCATTGC AGGTTGGCAC CTTACTTCCC TGGGATCCCCA 5227
GAGTTGGTCC AAGGAGGGAG AGTGGGTTCT CAATACGGTA CCAAAGATAT AATCACCTAG 5287
GTTTACAAAT ATTTTATAGGA CTCACGTAA CTCACATTTA TACAGCAGAA ATGCTATTTT 5347
GTATGCTGTT AAGTTTTTCT ATCTGTGTAC TTTTTTTTAA GGGAAAGATT TTAATATTAA 5407
ACCTGGTGCT TCTCACTCAC 5427

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Arg Leu Pro Gly Ala Met Pro Ala Leu Ala Leu Lys Gly Glu Leu
 1           5           10           15
Leu Leu Leu Ser Leu Leu Leu Leu Leu Glu Pro Gln Ile Ser Gln Gly
          20           25           30
Leu Val Val Thr Pro Pro Gly Pro Glu Leu Val Leu Asn Val Ser Ser
          35           40           45
Thr Phe Val Leu Thr Cys Ser Gly Ser Ala Pro Val Val Trp Glu Arg
          50           55           60
Met Ser Gln Glu Pro Pro Gln Glu Met Ala Lys Ala Gln Asp Gly Thr
        65           70           75           80
Phe Ser Ser Val Leu Thr Leu Thr Asn Leu Thr Gly Leu Asp Thr Gly
          85           90           95
Glu Tyr Phe Cys Thr His Asn Asp Ser Arg Gly Leu Glu Thr Asp Glu
          100          105          110
Arg Lys Arg Leu Tyr Ile Phe Val Pro Asp Pro Thr Val Gly Phe Leu
          115          120          125
Pro Asn Asp Ala Glu Glu Leu Phe Ile Phe Leu Thr Glu Ile Thr Glu
          130          135          140
Ile Thr Ile Pro Cys Arg Val Thr Asp Pro Gln Leu Val Val Thr Leu
          145          150          155          160
His Glu Lys Lys Gly Asp Val Ala Leu Pro Val Pro Tyr Asp His Gln
          165          170          175
Arg Gly Phe Ser Gly Ile Phe Glu Asp Arg Ser Tyr Ile Cys Lys Thr
          180          185          190

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Thr Ile Gly Asp Arg Glu Val Asp Ser Asp Ala Tyr Tyr Val Tyr Arg
 195 200 205
 Leu Gln Val Ser Ser Ile Asn Val Ser Val Asn Ala Val Gln Thr Val
 210 215 220
 Val Arg Gln Gly Glu Asn Ile Thr Leu Met Cys Ile Val Ile Gly Asn
 225 230 235 240
 Asp Val Val Asn Phe Glu Trp Thr Tyr Pro Arg Lys Glu Ser Gly Arg
 245 250 255
 Leu Val Glu Pro Val Thr Asp Phe Leu Leu Asp Met Pro Tyr His Ile
 260 265 270
 Arg Ser Ile Leu His Ile Pro Ser Ala Glu Leu Glu Asp Ser Gly Thr
 275 280 285
 Tyr Thr Cys Asn Val Thr Glu Ser Val Asn Asp His Gln Asp Glu Lys
 290 295 300
 Ala Ile Asn Ile Thr Val Val Glu Ser Gly Tyr Val Arg Leu Leu Gly
 305 310 315 320
 Glu Val Gly Thr Leu Gln Phe Ala Glu Leu His Arg Ser Arg Thr Leu
 325 330 335
 Gln Val Val Phe Glu Ala Tyr Pro Pro Pro Thr Val Leu Trp Phe Lys
 340 345 350
 Asp Asn Arg Thr Leu Gly Asp Ser Ser Ala Gly Glu Ile Ala Leu Ser
 355 360 365
 Thr Arg Asn Val Ser Glu Thr Arg Tyr Val Ser Glu Leu Thr Leu Val
 370 375 380
 Arg Val Lys Val Ala Glu Ala Gly His Tyr Thr Met Arg Ala Phe His
 385 390 395 400
 Glu Asp Ala Glu Val Gln Leu Ser Phe Gln Leu Gln Ile Asn Val Pro
 405 410 415
 Val Arg Val Leu Glu Leu Ser Glu Ser His Pro Asp Ser Gly Glu Gln
 420 425 430
 Thr Val Arg Cys Arg Gly Arg Gly Met Pro Gln Pro Asn Ile Ile Trp
 435 440 445
 Ser Ala Cys Arg Asp Leu Lys Arg Cys Pro Arg Glu Leu Pro Pro Thr
 450 455 460
 Leu Leu Gly Asn Ser Ser Glu Glu Glu Ser Gln Leu Glu Thr Asn Val
 465 470 475 480
 Thr Tyr Trp Glu Glu Glu Gln Glu Phe Glu Val Val Ser Thr Leu Arg
 485 490 495
 Leu Gln His Val Asp Arg Pro Leu Ser Val Arg Cys Thr Leu Arg Asn
 500 505 510
 Ala Val Gly Gln Asp Thr Gln Glu Val Ile Val Val Pro His Ser Leu
 515 520 525
 Pro Phe Lys Val Val Val Ile Ser Ala Ile Leu Ala Leu Val Val Leu
 530 535 540

Thr Ile Ile Ser Leu Ile Ile Leu Ile Met Leu Trp Gln Lys Lys Pro
 545 550 555 560
 Arg Tyr Glu Ile Arg Trp Lys Val Ile Glu Ser Val Ser Ser Asp Gly
 565 570 575
 His Glu Tyr Ile Tyr Val Asp Pro Met Gln Leu Pro Tyr Asp Ser Thr
 580 585 590
 Trp Glu Leu Pro Arg Asp Gln Leu Val Leu Gly Arg Thr Leu Gly Ser
 595 600 605
 Gly Ala Phe Gly Gln Val Val Glu Ala Thr Ala His Gly Leu Ser His
 610 615 620
 Ser Gln Ala Thr Met Lys Val Ala Val Lys Met Leu Lys Ser Thr Ala
 625 630 635 640
 Arg Ser Ser Glu Lys Gln Ala Leu Met Ser Glu Leu Lys Ile Met Ser
 645 650 655
 His Leu Gly Pro His Leu Asn Val Val Asn Leu Leu Gly Ala Cys Thr
 660 665 670
 Lys Gly Gly Pro Ile Tyr Ile Ile Thr Glu Tyr Cys Arg Tyr Gly Asp
 675 680 685
 Leu Val Asp Tyr Leu His Arg Asn Lys His Thr Phe Leu Gln His His
 690 695 700
 Ser Asp Lys Arg Arg Pro Pro Ser Ala Glu Leu Tyr Ser Asn Ala Leu
 705 710 715 720
 Pro Val Gly Leu Pro Leu Pro Ser His Val Ser Leu Thr Gly Glu Ser
 725 730 735
 Asp Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Val Asp Tyr Val
 740 745 750
 Pro Met Leu Asp Met Lys Gly Asp Val Lys Tyr Ala Asp Ile Glu Ser
 755 760 765
 Ser Asn Tyr Met Ala Pro Tyr Asp Asn Tyr Val Pro Ser Ala Pro Glu
 770 775 780
 Arg Thr Cys Arg Ala Thr Leu Ile Asn Glu Ser Pro Val Leu Ser Tyr
 785 790 795 800
 Met Asp Leu Val Gly Phe Ser Tyr Gln Val Ala Asn Gly Met Glu Phe
 805 810 815
 Leu Ala Ser Lys Asn Cys Val His Arg Asp Leu Ala Ala Arg Asn Val
 820 825 830
 Leu Ile Cys Glu Gly Lys Leu Val Lys Ile Cys Asp Phe Gly Leu Ala
 835 840 845
 Arg Asp Ile Met Arg Asp Ser Asn Tyr Ile Ser Lys Gly Ser Thr Phe
 850 855 860
 Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asn Ser Leu Tyr
 865 870 875 880
 Thr Thr Leu Ser Asp Val Trp Ser Phe Gly Ile Leu Leu Trp Glu Ile
 885 890 895

Phe Thr Leu Gly Gly Thr Pro Tyr Pro Glu L u-Pro Met Asn Glu Gln
 900 905 910
 Phe Tyr Asn Ala Ile Lys Arg Gly Tyr Arg Met Ala Gln Pro Ala His
 915 920 925
 Ala Ser Asp Glu Ile Tyr Glu Ile Met Gln Lys Cys Trp Glu Glu Lys
 930 935 940
 Phe Glu Ile Arg Pro Pro Phe Ser Gln Leu Val Leu Leu Leu Glu Arg
 945 950 955 960
 Leu Leu Gly Glu Gly Tyr Lys Lys Lys Tyr Gln Gln Val Asp Glu Glu
 965 970 975
 Phe Leu Arg Ser Asp His Pro Ala Ile Leu Arg Ser Gln Ala Arg Leu
 980 985 990
 Pro Gly Phe His Gly Leu Arg Ser Pro Leu Asp Thr Ser Ser Val Leu
 995 1000 1005
 Tyr Thr Ala Val Gln Pro Asn Glu Gly Asp Asn Asp Tyr Ile Ile Pro
 1010 1015 1020
 Leu Pro Asp Pro Lys Pro Glu Val Ala Asp Glu Gly Pro Leu Glu Gly
 1025 1030 1035 1040
 Ser Pro Ser Leu Ala Ser Ser Thr Leu Asn Glu Val Asn Thr Ser Ser
 1045 1050 1055
 Thr Ile Ser Cys Asp Ser Pro Leu Glu Pro Gln Asp Glu Pro Glu Pro
 1060 1065 1070
 Glu Pro Gln Leu Glu Leu Gln Val Glu Pro Glu Pro Glu Leu Glu Gln
 1075 1080 1085
 Leu Pro Asp Ser Gly Cys Pro Ala Pro Arg Ala Glu Ala Glu Asp Ser
 1090 1095 1100
 Phe Leu *
 1105

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Peptide Y719"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro
 1 5 10 15
 Met Leu Asp Met
 20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Peptide Y719P. Contains a phosphate group at position 14."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro
 1 5 10 15

Met Leu Asp Met
 20

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..20
- (D) OTHER INFORMATION: /note= "Peptide Y708P. Contains a phosphate group at position 3."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro
 1 5 10 15

Met Leu Asp Met
 20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..17
- (D) OTHER INFORMATION: /note= "Peptide Y719P short."

Contains a phosphate group at position 11."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro Met Leu Asp
1 5 10 15

Met

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..13

(D) OTHER INFORMATION: /note= "Peptide Y708P short.
Contains a phosphate group at position 3."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp
1 5 10

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..20

(D) OTHER INFORMATION: /note= "Peptide Y708P/F719.
Contains a phosphate group at position 3."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Phe Val Pro
1 5 10 15

Met Leu Asp Met
20

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..20

(D) OTHER INFORMATION: /note= "Peptide Y708/Y719P.

Contains a phosphate group at position 14."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly Gly Phe Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro
1 5 10 15

Met Leu Asp Met
20

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..20

(D) OTHER INFORMATION: /note= "Peptide Y708P/Y719P.

Contains phosphate group at positions 3 & 14"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Gly Tyr Met Asp Met Ser Lys Asp Glu Ser Ile Asp Tyr Val Pro
1 5 10 15

Met Leu Asp Met
20

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..20

(D) OTHER INFORMATION: /note= "Peptide Y719P scrambled.

Contains a phosphate group at position 15."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Met Asp Ile Lys Val Pro Met Asp Glu Tyr Met Ser Asp Tyr Ser
1 5 10 15

Asp Leu Gly Gly
20

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURES:

- (D) OTHER INFORMATION: /note= "N is A, C, G, or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTTSCGNGCN GCCAGNTCSC GNTG